Fig. 1

| 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 |

HI N   H   N EI I M   B   H N A E N   N B B   H   M I   M   E H/B EJ M   K   Kbp

E1
E2
E3   EMBL3

P1   P2   PCR

ORF280   ORF277   ORF217   ORF467   ORF80   ORF232

sll0524   slr1895   sll1300   slr1515   Ribosome binding   O-acetylhomoserine
YZ02-myctu   ICC, Y128-SYNP6 YGGH transporters   factor A   sulfhydrylase

Fig. 4a

A. Wild type

- LC-HCO$_3^-$
- LC-CO$_2$
- HC-HCO$_3^-$
- HC-CO$_2$

y-axis: μmol Ci / mg chl · h
x-axis: HCO$_3^-$ concentration, mM

Fig. 4b

B. Mutant IL-2

- LC-HCO$_3^-$
- LC-CO$_2$
- HC-HCO$_3^-$
- HC-CO$_2$

y-axis: μmol Ci / mg chl · h
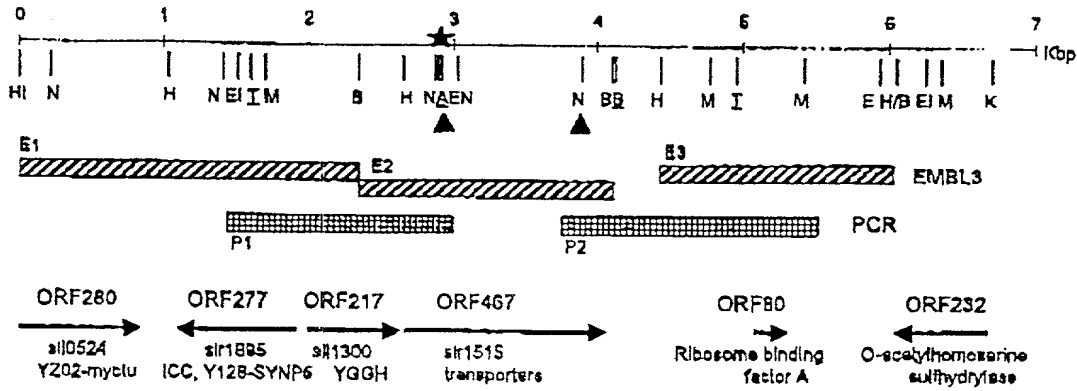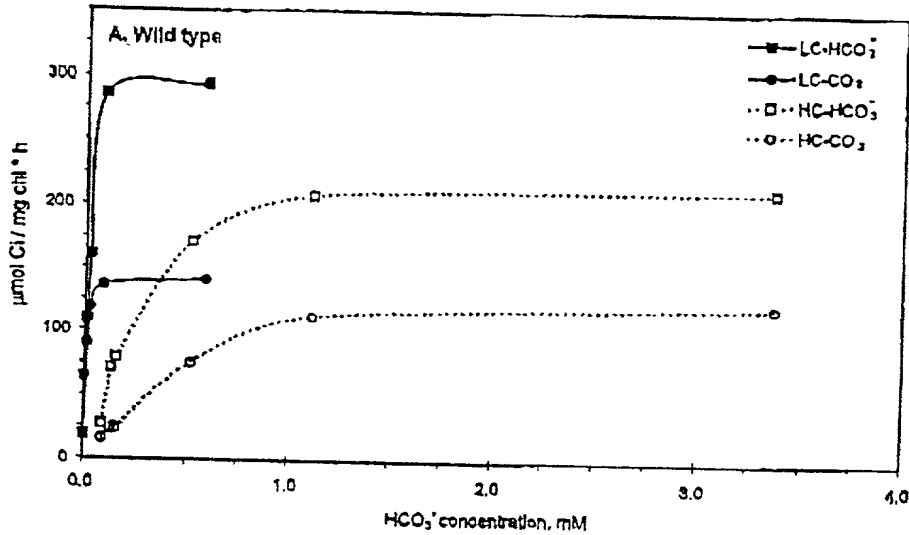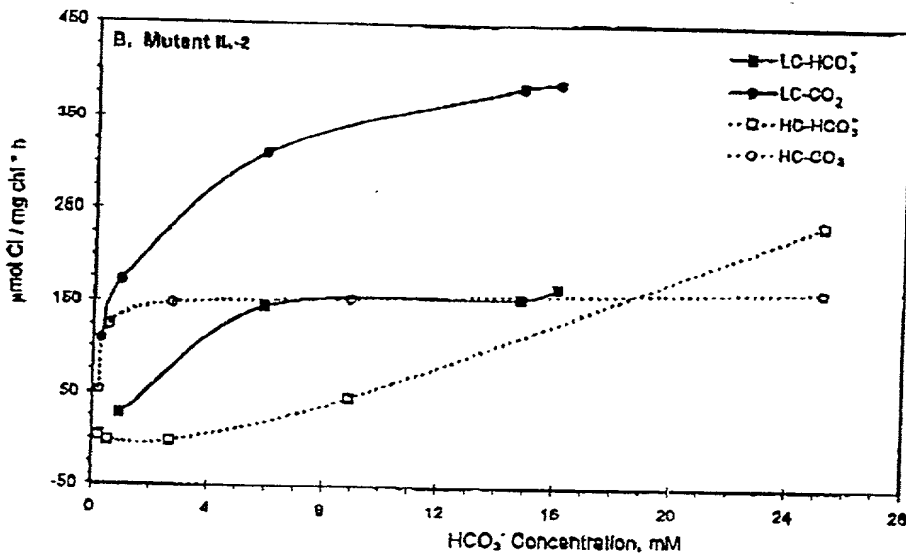x-axis: HCO$_3^-$ Concentration, mM

FIGURE 2

```
ICTB : 1    ATGACTGTCTGGCAAACTCTGACTTTTGCCCATTACCAACCCCAACAGTGGGGCCACAGC 60 (SEQ ID NO:2)
            ||  || ||||||| | | |||| |||| || | || |   ||||| | ||||||| ||
SLR  : 13   ATCTCTATCTGGCGATCGCTGATGTTTGGCGGTTTTTCCCCCCAGGAATGGGGCCGGGGC 72 (SEQ ID NO:4)


ICTB : 61   AGTTTCTTGCATCGGCTGTTTGGCAGCCTGC-GAGCTTGGCGGGCCTCCAGCCAGCTGTT 119
            ||| |  | ||||||  || | ||| |    | || |||| | ||    | ||   ||| |
SLR  : 73   AGTGTGCTCCATCGTTTGGTGGGCTGGGGACAGAG-TTGGATACAGGCTAGTGTGCTCTG 131


ICTB : 120  GGTTTGGTCTGAGGCACTGGGT--GGCTTCTTGCTTGCTGTCGTCTACGGTTCGGCTCCG 177
            |     |   |||||| ||||| |||| || | | ||  | |     |  ||||||||
SLR  : 132  GCCCCACTTCGAGGCATTGGGTACGGCT-CTAG-TGGCAATAATTTTTATTGCGGCTCCC 189


ICTB : 178  TTTGTGCCCAGTTCCGCCCTAGGGTTGGGGCTAGCCGCGATCGCG-GCCTATTGGGCCCT 236
            ||    |||  ||    | || |   | || ||  |  | |||| |||||| || |
SLR  : 190  TTCACCTCCACCACCATGTTGGGCATTTTTTAT-GCTGCTCTGTGGAGCCTTTTGGGCTCT 248


ICTB : 237  GCTCTCGCTGACAGATATCGATCTGCGGCAAGCA---ACCCCCATTCACTGGCTGGTGCT 293
            |||  | | | ||| | | | | || | |   || |||||| ||   | || |
SLR  : 249  GCTGACCTTTGCTGAT--CAACCAG-GGAAGGGTTTGACTCCCATCCATGTTTTAGTTTT 305


ICTB : 294  GCTCTACTGGGGCGTCGATGCCCTAGCAACGGGACTCTCACCCGTACGCGCTGCAGCTTT 353
              ||||||| ||  |      || | ||   |||| | || || ||| |       || ||
SLR  : 306  TGCCTACTGGTGCATTTCGGCGATCGCCGTGGGATTTTCTCCGGTAAAAATGGCGGCGGC 365


ICTB : 354  AGTTGGGCTAGCCAAACTGAC-GCTC-TACCTGTTGGTTTTTGCCCTAGCGGCTCGGGTT 411
            ||| |||| ||| | |  ||| |   | || |||| | | | |||||  || |
SLR  : 366  GTCGGGGTTAGCGAAATTAACAGCTAATTTATGTCTGTTCTAC--TGGCGGCGAGGTTA 423


ICTB : 412  CTCCGCAATCCCCGTCTGC-GATCGCTGCTGTTCTCGGTCGTCGTGATCACATCGCTTTT 470
            | |  ||   |     ||| | ||| | | | |   |  | | || | |   || || ||
SLR  : 424  TTGCAAAACAAACAATGGTTGAAC-CGGTTAGTAACCGTTGTTTTACTGGTAGGGCTATT 482


ICTB : 471  TGTCAGTGTCTACGGCCTCAACCAATGGATCTACGGCGTTGAAGAGCTGGCGACTTGGGT 530
             ||  |    |||||  ||    ||| |  | | |||| || ||| || | || ||||||
SLR  : 483  GGTGGGGAGTTACGGTCTGCGACAACAGGTGGACGGGGTAGAACAGTTAGCCACTTGGAA 542


ICTB : 531  GGATCGCAACTCGGTTGCCGACTTCACCTCACGGGTTTACAGCTATCTGGGCAACCCCAA 590
            || | ||  |||        || |   || | ||||| || |||| | | || || |||||
SLR  : 543  TGACCCCACCTCTACCTTGGCCCAGGCCACTAGGGTATATAGCTTTTTAGGTAATCCCAA 602


ICTB : 591  CCTGCTGGCTGCTTATCTGGTGCCGACGACTGCCTTTT-CTGCAGCAGCGATCGGGGTGT 649
            ||  |||| |||||| |||||||| ||||||| | ||| |   ||  ||  || | ||| |
SLR  : 603  TCTCTTGGCGGCTTACCTGGTGCCCATGACGGGTTTGAGCTTGAGT-GCCCTGGTGGTAT 661


ICTB : 650  GGCGCGGCTGGCTCCCCAAGCTGCTGGCGATCG-CTGCGACAGGTGCGAGCAGCTTATGT 708
            ||||  | |||  |||| | ||||||||||| ||  | |  |  |    || | |  | |||
SLR  : 662  GGCGACGGTGGTGGCCCAAACTGCTGG-GAGCAACCATGGTGATTGTTAACCTACTCTGT 720


ICTB : 709  CTGATCCTCACCTACAGTCGCGGTGGCTGGCTGGGTTTTGTCGCCATGATTTTTGTCTGG 768
            ||  |  | |||  | || || || || |   | | |||||  ||  ||  |  || |
SLR  : 721  CTCTTTTTTACCCAGAGCCGGGGCGGTTGGCTAGCAGTGCTGGCCCTGGGAGCTACCTTC 780


ICTB : 769  GCGTTATTAGGGCTCTACTGGTTTCAACCCCGTCTACCCGCACCCTGGCGACGCTGGCTA 828
             |     |  |  || ||||| |   ||||| |  ||||| | |||| |    |||| |||
SLR  : 781  CTGGCCCTTTGTTACTTCTGGTGGTTACCCCAATTACCCAAATTTTGGCAACGGTGGTCT 840


ICTB : 829  TTCCCAGTCGTATTGGGTGGACTAGTCGCGGTGCTCTT-GGTGGCGGTGCTTGGACT--- 884
            || || | |    | | | ||  | |  || || |||| | || ||||| || || | || |
SLR  : 841  TTGCCCCTGGC----GATCGCC--GTGGCGGTTATATTAGGTGGGGGAGCGTTGATTGCG 894


ICTB : 885  -TG-AGCCGTTGCGCGTGCGCGTGTTGAGCATCTTTGTGGGGCGTGAAGACAGCAGCAAC 942
            || | ||| || || |     |  ||||||| ||||  ||||| |||||||||||||| ||
SLR  : 895  GTGGAACCGATTCGACTCAGGGCCATGAGCATTTTTGCTGGGCGGGAAGACAGCAGTAAT 954
```

FIGURE 2 (CONTINUED)

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ICTB : 943   AACTTCCGGATCAATGTCTGGCTGGCGGTGCTGCAGATGATTCAAGATCGGCCTTGGCTG 1002
             || ||||| |||||||| |||  |  |||     ||||| | ||  || |||     |
SLR  : 955   AATTTCCGCATCAATGTTTGGGAAGGGGTAAAAGCCATGATCCGAGCCCGCCCTATCATT 1014


ICTB : 1003  GGCATCGGCCCCGGCAATACCGCCTTTAACCTGGTTTATCCCCTCTATCAACAGGCGCGC 1062
             ||||| ||||| || ||     |||||||||| |||||||  ||||   | | | |||
SLR  : 1015  GGCATTGGCCCAGGTAACGAAGCCTTTAACCAAATTTATCCTTACTATATGCGGCCCCGC 1074


ICTB : 1063  TTTACGGCGTTGAGCGCCTACTCCGTCCCGCTGGAAGTCGCGGTTGAGGGCGGACTACTG 1122
             || || ||  ||||  |||||| |||  |   || ||| |  ||| ||   || ||| |
SLR  : 1075  TTCACCGCCCTGAGTGCCTATTCCATTTACCTAGAAATTTTGGTGGAAACGGGTGTAGTT 1134


ICTB : 1123  GGCTTGA-CGGCCTTCGCTTGGCTGCT-GCTGGTCACGGCGGTGACGGCGGTGCGGCAGG 1180
             |! || | |  | | | ||||||| | || | |  |   || | ||| ||    | ||
SLR  : 1135  GGTTTTACCTGTATGCTC-TGGCTGTTGGCCGTTACCCTAGGCAAAGGC-GTAGAACTGG 1192


ICTB : 1181  TGAGCCGACTGCGGCGCGATCGCAATCCCC--AAGCCTTTTGGTTGATGGCTAGCTTGGC 1238
             | |  || ||| || | | | |  ||||  ||| ||| | | ||| | ||||    || ||
SLR  : 1193  TTAAACG-CTGTCGC-CAAACCCTCGCCCCGGAAGGCATCTGGATTATGGGGGCTTTAGC 1250


ICTB : 1239  CGGTTTGGCAGGAATGCTGGGTCACGGTCTGTTTGATACCGTGCTCTATCGACCGGAAGC⁻1298
             |   |   || || ||  ||||| || | ||||| || | |||||| ||  || || ||  |
SLR  : 1251  GGCGATCATCGGTTTGTTGGTCCACGGCATGGTAGATACAGTCTGGTACCGTCCCCCGGT 1310


ICTB : 1299  CAGTACGCTCTGGTGGCTCTGTATTGG--ÀGCGATCGCGAGTTTCTGG--CAGC-CCCAA 1353
             || || | |||||| |  || ||| | | | || |  | | |||   ||| |||| ||||
SLR  : 1311  GAGCACTTTGTGGTGG-TTGCTAGTGGCCATTG-TTGCTAGTCAGTGGGCCAGCGCCCAG 1368


ICTB : 1354  CCTTCCAAGCAACTCCCTCCAGAAGCCGAGCATTCAGACGAA 1395
              |     | |   | |  |||| || || |||  ||
SLR  : 1369  GCCCGTTTGGAGGCCAGTAAAGAA---GAAAATGAGGACAAA 1407
```

FIGURE 3

```
ICTB  :   1  MTVWQTLTFAHYQPQQWGHSSFLHRLFGSLRAWRASSQLLVWSEALGGFLLAVVYGSAPF  60
             +++W++L F + PQ+WG S LHRL G ++W +S L   EALG L+A+++ +APF
SLR   :   5  ISIWRSLMFGGFSPQEWGRGSVLHRLVGWGQSWIQASVLWPHFEALGTALVAIIFIAAPF  64

ICTB  :  61  VPSSALGLGLAAIAAYWALLSLTDIDLRQATPIHWLVLLYWGVDALATGLSPVRAAALVG  120
             ++ LG+ +  A+WALL+ D  + TPIH LV  YW + A+A G SPV+ AA   G
SLR   :  65  TSTTMLGIFMLLCGAFWALLTFADQPGKGLTPIHVLVFAYWCISAIAVGFSPVKMAAASG  124

ICTB  : 121  LAKLTLYLLVFALAARVLRNPRLRSLLFSVVVITSLFVSVYGLNQWIYGVEELATWVDRN  180
             LAKLT  L +F LAAR+L+N +  + L +VV++  L V  YGL Q + GVE+LATW D
SLR   : 125  LAKLTANLCLFLLAARLLQNKQWLNRLVTVVLLVGLLVGSYGLRQQVDGVEQLATWNDPT  184

ICTB  : 181  SVADFTSRVYSYLGNPNLLAAYLVPTTAFSAAAIGVWRGWLPKLLAIAATGASSLCLILT  240
             S     +RVYS+LGNPNLLAAYLVP T  S +A+ VWR W PKLL      + LCL  T
SLR   : 185  STLAQATRVYSFLGNPNLLAAYLVPMTGLSLSALVVWRRWWPKLLGATMVIVNLLCLFFT  244

ICTB  : 241  YSRGGWLGFVAMIFVWALLGLYWFQPRLPAPWRRWLFPVVLGGLVAVLLVAVLGLEPLRV  300
             SRGGWL +A+   + L +W+ P+LP  W+RW P+ +   V +  A++ +EP+R+
SLR   : 245  QSRGGWLAVLALGATFLALCYFWWLPQLPKFWQRWSLPLAIAVAVILGGGALIAVEPIRL  304

ICTB  : 301  RVLSIFVGREDSSNNFRINVWLAVLQMIQDRPWLGIGPGNTAFNLVYPLYQQARFTALSA  360
             R +SIF GREDSSNNFRINVW  V  MI+ RP +GIGPGN AFN +YP Y + RFTALSA
SLR   : 305  RAMSIFAGREDSSNNFRINVWEGVKAMIRARPIIGIGPGNEAFNQIYPYYMRPRFTALSA  364

ICTB  : 361  YSVPLEVAVEGGLLGLTAFAWLLLVTAVTAVRQVSRLRRDRNPQAFWLMASLAGLAGMLG  420
             YS+ LE+ VE G++G T  WLL VT    V  V R+   P+ W+M +LA  G+L
SLR   : 365  YSIYLEILVETGVVGFTCMLWLLAVTLGKGVELVKRCRQTLAPEGIWIMGALAAIIGLLV  424

ICTB  : 421  HGLFDTVLYRPEASTLWWLCIGAIASFWQPQPSKQLPPEAEHSDEKM  467
             HG+ DTV YRP  STLWWL + +AS W  ++    + E+ D+ +
SLR   : 425  HGMVDTVWYRPPVSTLWWLLVAIVASQWASAQARLEASKEENEDKPL  471
```

Fig. 5

```
Wild type        GGGCT-AGCCGCGATCGCGGCCTATTGGGCCC  (SEQ ID NO:6)
IL-2 ApaI side   GGGCT-AG--G-GATCGC-GCCTATTGGGCCC  (SEQ ID NO:7)
IL-2 BamHI side  GGGCTCA-----GATCGC-GCCTATTGGGCCC  (SEQ ID NO:8)
IctB              G  L  A  A  I  A  A  Y  W  A  L  (SEQ ID NO:9)
```

Fig. 6

Transgenic
35S:ictB

WT   A   B   C